

2848-56-PCT.ST25.txt
SEQUENCE LISTING

<110> Hutton, John C.
O'Brien, Richard
Davidson, Howard
Hackl, Seija

<120> Use of Islet Glucose-6-Phosphatase Related Protein as a Diagnostic Tool and
Therapeutic Target for Autoimmune Diabetes

<130> 2848-56-PCT

<150> US 60/505317

<151> 2003-09-22

<160> 7

<170> PatentIn version 3.1

<210> 1

<211> 1068

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1065)

<223>

<400> 1

atg gat ttc ctt cac agg aat gga gtg ctc ata att cag cat ttg cag	48
Met Asp Phe Leu His Arg Asn Gly Val Leu Ile Ile Gln His Leu Gln	
1 5 10 15	
aag gac tac cga gct tac tac act ttt cta aat ttt atg tcc aat gtt	96
Lys Asp Tyr Arg Ala Tyr Tyr Thr Phe Leu Asn Phe Met Ser Asn Val	
20 25 30	
gga gac ccc agg aat atc ttt ttc att tat ttt cca ctt tgt ttt caa	144
Gly Asp Pro Arg Asn Ile Phe Phe Ile Tyr Phe Pro Leu Cys Phe Gln	
35 40 45	
ttt aat cag aca gtt gga acc aag atg ata tgg gta gca gtc att ggg	192
Phe Asn Gln Thr Val Gly Thr Lys Met Ile Trp Val Ala Val Ile Gly	
50 55 60	
gat tgg tta aat ctt ata ttt aaa tgg ata tta ttt ggt cat cga cct	240
Asp Trp Leu Asn Leu Ile Phe Lys Trp Ile Leu Phe Gly His Arg Pro	
65 70 75 80	
tac tgg tgg gtc caa gaa act cag att tac cca aat cac tca agt cca	288
Tyr Trp Trp Val Gln Glu Thr Gln Ile Tyr Pro Asn His Ser Ser Pro	
85 90 95	
tgc ctt gaa cag ttc cct act aca tgt gaa aca ggt cca gga agt cca	336
Cys Leu Glu Gln Phe Pro Thr Thr Cys Glu Thr Gly Pro Gly Ser Pro	
100 105 110	
tct ggc cat gca atg ggc gca tcc tgt gtc tgg tat gtc atg gta acc	384
Ser Gly His Ala Met Gly Ala Ser Cys Val Trp Tyr Val Met Val Thr	
115 120 125	
gct gcc ctg agc cac act gtc tgt ggg atg gat aag ttc tct atc act	432

2848-56-PCT.ST25.txt

Ala	Ala	Leu	Ser	His	Thr	Val	Cys	Gly	Met	Asp	Lys	Phe	Ser	Ile	Thr		
130						135					140						
ctg	cac	aga	ctg	acc	tgg	tca	ttt	ctt	tgg	agt	gtt	ttt	tgg	ttg	att		480
Leu	His	Arg	Leu	Thr	Trp	Ser	Phe	Leu	Trp	Ser	Val	Phe	Trp	Leu	Ile		
145					150					155					160		
caa	atc	agt	gtc	tgc	atc	tcc	aga	gta	ttc	ata	gca	aca	cat	ttt	cct		528
Gln	Ile	Ser	Val	Cys	Ile	Ser	Arg	Val	Phe	Ile	Ala	Thr	His	Phe	Pro		
				165					170					175			
cat	caa	gtt	att	ctt	gga	gta	att	ggg	ggc	atg	ctg	gtg	gca	gag	gcc		576
His	Gln	Val	Ile	Leu	Gly	Val	Ile	Gly	Gly	Met	Leu	Val	Ala	Glu	Ala		
			180					185					190				
ttt	gaa	cac	act	cca	ggc	atc	caa	acg	gcc	agt	ctg	ggc	aca	tac	ctg		624
Phe	Glu	His	Thr	Pro	Gly	Ile	Gln	Thr	Ala	Ser	Leu	Gly	Thr	Tyr	Leu		
		195					200					205					
aag	acc	aac	ctc	ttt	ctc	ttc	ctg	ttt	gca	gtt	ggc	ttt	tac	ctg	ctt		672
Lys	Thr	Asn	Leu	Phe	Leu	Phe	Leu	Phe	Ala	Val	Gly	Phe	Tyr	Leu	Leu		
	210					215					220						
ctt	agg	gtg	ctc	aac	att	gac	ctg	ctg	tgg	tcc	gtg	ccc	ata	gcc	aaa		720
Leu	Arg	Val	Leu	Asn	Ile	Asp	Leu	Leu	Trp	Ser	Val	Pro	Ile	Ala	Lys		
225					230					235					240		
aag	tgg	tgt	gct	aac	ccc	gac	tgg	atc	cac	att	gac	acc	acg	cct	ttt		768
Lys	Trp	Cys	Ala	Asn	Pro	Asp	Trp	Ile	His	Ile	Asp	Thr	Thr	Pro	Phe		
				245					250					255			
gct	gga	ctc	gtg	aga	aac	ctt	ggg	gtc	ctc	ttt	ggc	ttg	ggc	ttt	gca		816
Ala	Gly	Leu	Val	Arg	Asn	Leu	Gly	Val	Leu	Phe	Gly	Leu	Gly	Phe	Ala		
			260					265					270				
atc	aac	tca	gag	atg	ttc	ctc	ctg	agc	tgc	cga	ggg	gga	aat	aac	tac		864
Ile	Asn	Ser	Glu	Met	Phe	Leu	Leu	Ser	Cys	Arg	Gly	Gly	Asn	Asn	Tyr		
		275					280					285					
aca	ctg	agc	ttc	cgg	ttg	ctc	tgt	gcc	ttg	acc	tca	ttg	aca	ata	ctg		912
Thr	Leu	Ser	Phe	Arg	Leu	Leu	Cys	Ala	Leu	Thr	Ser	Leu	Thr	Ile	Leu		
	290					295					300						
cag	ctc	tac	cat	ttc	ctc	cag	atc	ccg	act	cac	gaa	gag	cat	tta	ttt		960
Gln	Leu	Tyr	His	Phe	Leu	Gln	Ile	Pro	Thr	His	Glu	Glu	His	Leu	Phe		
305					310					315					320		
tat	gtg	ctg	tct	ttt	tgt	aaa	agt	gca	tcc	att	ccc	cta	act	gtg	gtt		1008
Tyr	Val	Leu	Ser	Phe	Cys	Lys	Ser	Ala	Ser	Ile	Pro	Leu	Thr	Val	Val		
				325					330					335			
gct	ttc	att	ccc	tac	tct	gtt	cat	atg	tta	atg	aaa	caa	agc	gga	aag		1056
Ala	Phe	Ile	Pro	Tyr	Ser	Val	His	Met	Leu	Met	Lys	Gln	Ser	Gly	Lys		
			340					345					350				
aag	agt	cag	tag														1068
Lys	Ser	Gln															
		355															

<210> 2
 <211> 355
 <212> PRT

<213> Homo sapiens

<400> 2

Met Asp Phe Leu His Arg Asn Gly Val Leu Ile Ile Gln His Leu Gln
 1 5 10 15

Lys Asp Tyr Arg Ala Tyr Tyr Thr Phe Leu Asn Phe Met Ser Asn Val
 20 25 30

Gly Asp Pro Arg Asn Ile Phe Phe Ile Tyr Phe Pro Leu Cys Phe Gln
 35 40 45

Phe Asn Gln Thr Val Gly Thr Lys Met Ile Trp Val Ala Val Ile Gly
 50 55 60

Asp Trp Leu Asn Leu Ile Phe Lys Trp Ile Leu Phe Gly His Arg Pro
 65 70 75 80

Tyr Trp Trp Val Gln Glu Thr Gln Ile Tyr Pro Asn His Ser Ser Pro
 85 90 95

Cys Leu Glu Gln Phe Pro Thr Thr Cys Glu Thr Gly Pro Gly Ser Pro
 100 105 110

Ser Gly His Ala Met Gly Ala Ser Cys Val Trp Tyr Val Met Val Thr
 115 120 125

Ala Ala Leu Ser His Thr Val Cys Gly Met Asp Lys Phe Ser Ile Thr
 130 135 140

Leu His Arg Leu Thr Trp Ser Phe Leu Trp Ser Val Phe Trp Leu Ile
 145 150 155 160

Gln Ile Ser Val Cys Ile Ser Arg Val Phe Ile Ala Thr His Phe Pro
 165 170 175

His Gln Val Ile Leu Gly Val Ile Gly Gly Met Leu Val Ala Glu Ala
 180 185 190

Phe Glu His Thr Pro Gly Ile Gln Thr Ala Ser Leu Gly Thr Tyr Leu
 195 200 205

Lys Thr Asn Leu Phe Leu Phe Leu Phe Ala Val Gly Phe Tyr Leu Leu
 210 215 220

Leu Arg Val Leu Asn Ile Asp Leu Leu Trp Ser Val Pro Ile Ala Lys
 225 230 235 240

2848-56-PCT.ST25.txt

Lys Trp Cys Ala Asn Pro Asp Trp Ile His Ile Asp Thr Thr Pro Phe
245 250 255

Ala Gly Leu Val Arg Asn Leu Gly Val Leu Phe Gly Leu Gly Phe Ala
260 265 270

Ile Asn Ser Glu Met Phe Leu Leu Ser Cys Arg Gly Gly Asn Asn Tyr
275 280 285

Thr Leu Ser Phe Arg Leu Leu Cys Ala Leu Thr Ser Leu Thr Ile Leu
290 295 300

Gln Leu Tyr His Phe Leu Gln Ile Pro Thr His Glu Glu His Leu Phe
305 310 315 320

Tyr Val Leu Ser Phe Cys Lys Ser Ala Ser Ile Pro Leu Thr Val Val
325 330 335

Ala Phe Ile Pro Tyr Ser Val His Met Leu Met Lys Gln Ser Gly Lys
340 345 350

Lys Ser Gln
355

<210> 3
<211> 1901
<212> DNA
<213> Mus. musculus

<220>
<221> CDS
<222> (63)..(1127)
<223>

<400> 3
tagagacagt gggacacagg gccctgcagt tccacctgct tcatgcttag acctgcatca 60

ag atg gat ttc ctt cat agg agt gga gtg ctt att att cat cat ctg 107
Met Asp Phe Leu His Arg Ser Gly Val Leu Ile Ile His His Leu
1 5 10 15

cag gag gac tac cgg act tac tat ggt ttt cta aat ttt atg tcc aat 155
Gln Glu Asp Tyr Arg Thr Tyr Tyr Gly Phe Leu Asn Phe Met Ser Asn
20 25 30

gtt gga gac ccc cga aat atc ttt tct att tac ttc cca ctt tgg ttt 203
Val Gly Asp Pro Arg Asn Ile Phe Ser Ile Tyr Phe Pro Leu Trp Phe
35 40 45

cag ttg aat cag aat gtt gga acc aag atg atc tgg gta gcg gtc ata 251
Gln Leu Asn Gln Asn Val Gly Thr Lys Met Ile Trp Val Ala Val Ile
50 55 60

ggg gac tgg ttc aat ctc ata ttt aaa tgg ata ttg ttt ggc cat cgt 299

2848-56-PCT.ST25.txt

Gly 65	Asp	Trp	Phe	Asn	Leu	Ile 70	Phe	Lys	Trp	Ile 75	Leu	Phe	Gly	His	Arg	
cct Pro 80	tac Tyr	tgg Trp	tgg Trp	ata Ile	caa Gln 85	gaa Glu	act Thr	gag Glu	att Ile	tat Tyr 90	cca Pro	aat Asn	cat His	tca Ser	agc Ser 95	347
cca Pro	tgt Cys	ctt Leu	gag Glu	cag Gln 100	ttt Phe	cct Pro	act Thr	acg Thr	tgt Cys 105	gaa Glu	aca Thr	ggc Gly	cca Pro	gga Gly 110	agt Ser	395
cca Pro	tct Ser	ggc Gly	cac His 115	gca Ala	atg Met	ggc Gly	tca Ser	tcg Ser 120	tgc Cys	gtc Val	tgg Trp	tat Tyr	gtc Val 125	atg Met	gta Val	443
aca Thr	gct Ala	gcc Ala 130	cta Leu	agc Ser	tac Tyr	acc Thr	atc Ile 135	agc Ser	cgg Arg	atg Met	gag Glu	gag Glu 140	tcc Ser	tct Ser	gtc Val	491
act Thr	ctg Leu 145	cac His	aga Arg	ctg Leu	acc Thr	tgg Trp 150	tcc Ser	ttt Phe	ctg Leu	tgg Trp	agt Ser 155	gtt Val	ttc Phe	tgg Trp	ttg Leu	539
att Ile 160	caa Gln	atc Ile	agc Ser	gtc Val	tgc Cys 165	atc Ile	tca Ser	aga Arg	gta Val	ttc Phe 170	ata Ile	gcc Ala	aca Thr	cat His	ttc Phe 175	587
ccc Pro	cat His	cag Gln	gtc Val	att Ile 180	ctt Leu	gga Gly	gtg Val	att Ile	ggt Gly 185	ggg Gly	atg Met	cta Leu	gta Val	gcc Ala 190	gag Glu	635
gcc Ala	ttt Phe	gaa Glu	cac His 195	act Thr	cca Pro	gga Gly	gtc Val	cac His 200	atg Met	gcc Ala	agc Ser	ttg Leu	agt Ser 205	gtg Val	tac Tyr	683
ctg Leu	aag Lys	acc Thr 210	aac Asn	gtc Val	ttc Phe	ctc Leu	ttc Phe 215	ctg Leu	ttt Phe	gcc Ala	ctc Leu	ggc Gly 220	ttt Phe	tac Tyr	ctg Leu	731
ctt Leu 225	ctc Leu	cga Arg	ctg Leu	ttc Phe	ggt Gly	att Ile 230	gac Asp	ctg Leu	ctg Leu	tgg Trp	tcc Ser 235	gtg Val	ccc Pro	atc Ile	gcc Ala	779
aaa Lys 240	aag Lys	tgg Trp	tgt Cys	gcc Ala	aac Asn 245	cca Pro	gac Asp	tgg Trp	atc Ile	cac His 250	att Ile	gac Asp	agc Ser	acg Thr	cct Pro 255	827
ttt Phe	gct Ala	gga Gly	ctc Leu	gtg Val 260	aga Arg	aac Asn	ctc Leu	ggg Gly	gtc Val 265	ctc Leu	ttt Phe	ggc Gly	ttg Leu	ggt Gly 270	ttc Phe	875
gcc Ala	atc Ile	aac Asn 275	tca Ser	gaa Glu	atg Met	ttc Phe	ctt Leu	cgg Arg 280	agc Ser	tgc Cys	cag Gln	gga Gly	gaa Glu 285	aat Asn	ggc Gly	923
acc Thr	aag Lys	ccg Pro 290	agc Ser	ttc Phe	cgc Arg	ttg Leu	ctc Leu 295	tgt Cys	gct Ala	ctg Leu	acc Thr	tca Ser 300	ctg Leu	acc Thr	aca Thr	971
atg Met 305	caa Gln	ctt Leu	tat Tyr	cgc Arg	ttc Phe	atc Ile 310	aag Lys	atc Ile	ccg Pro	act Thr	cac His 315	gcg Ala	gaa Glu	cct Pro	tta Leu	1019

2848-56-PCT.ST25.txt

ttt tac ctg ttg tct ttc tgt aaa agt gcg tcc atc ccc ctg atg gtg 1067
 Phe Tyr Leu Leu Ser Phe Cys Lys Ser Ala Ser Ile Pro Leu Met Val
 320 325 330 335
 gtg gct cta att ccc tac tgt gta cat atg tta atg aga ccc ggt gac 1115
 Val Ala Leu Ile Pro Tyr Cys Val His Met Leu Met Arg Pro Gly Asp
 340 345 350
 aag aag act aaa tagagctgca gtgccctgtg gtctgaggat cacctacttt 1167
 Lys Lys Thr Lys
 355
 ctgtttttcct caatagagcc acagcacaga gactgggagc gtctctacag aggtcacacc 1227
 atgatgacca aaggctcctgc tccaccccaca gacatgttta gtctgctttc caagtggcat 1287
 ttaaaaaata acagtattta accagaaagt ccatattttc ttgacaaaac tgacaatacg 1347
 gtaacatatg agagatggta taacccatgt aaagacagtt gacaggggct ggatgcttac 1407
 attccagtta gcagaaagac tccttctaata catagtattt agcagtcaac aaaacccccca 1467
 ggagctgatg tttctatcat cttaaagtct ggctacttca ggctcctgtg gaccacttag 1527
 aagtgaccac ggtctacttt tacttttagg agtcaattct ttcaaaattc tcatgtatca 1587
 gataaggaaa tagaggtttg ttcagatcaa gtaacttgac tgtaatagtg caggggttgaa 1647
 accagagttg gaacacaagg cttctgatac atatatctct ataagaatgc tttctttcct 1707
 tcttttttagg gagttaaaaa aaaagagcaa atgcatgtat ttaaaatcta tgtttgccat 1767
 ctaaaacacc catcttttca gaaatggcat tggaatgcta cattctgctt gacttatgct 1827
 cagagtacag tgtcttttcc aggctagcaa tggctgtata tatttcaata aacgctgctg 1887
 aaaacaaccc actg 1901

<210> 4
 <211> 355
 <212> PRT
 <213> Mus musculus

<400> 4

Met Asp Phe Leu His Arg Ser Gly Val Leu Ile Ile His His Leu Gln
1 5 10 15

Glu Asp Tyr Arg Thr Tyr Tyr Gly Phe Leu Asn Phe Met Ser Asn Val
20 25 30

Gly Asp Pro Arg Asn Ile Phe Ser Ile Tyr Phe Pro Leu Trp Phe Gln
35 40 45

Leu Asn Gln Asn Val Gly Thr Lys Met Ile Trp Val Ala Val Ile Gly
50 55 60

Asp Trp Phe Asn Leu Ile Phe Lys Trp Ile Leu Phe Gly His Arg Pro

65		70		75		80									
Tyr	Trp	Trp	Ile	Gln	Glu	Thr	Glu	Ile	Tyr	Pro	Asn	His	Ser	Ser	Pro
			85						90					95	
Cys	Leu	Glu	Gln	Phe	Pro	Thr	Thr	Cys	Glu	Thr	Gly	Pro	Gly	Ser	Pro
			100					105					110		
Ser	Gly	His	Ala	Met	Gly	Ser	Ser	Cys	Val	Trp	Tyr	Val	Met	Val	Thr
		115					120					125			
Ala	Ala	Leu	Ser	Tyr	Thr	Ile	Ser	Arg	Met	Glu	Glu	Ser	Ser	Val	Thr
	130					135					140				
Leu	His	Arg	Leu	Thr	Trp	Ser	Phe	Leu	Trp	Ser	Val	Phe	Trp	Leu	Ile
145					150					155					160
Gln	Ile	Ser	Val	Cys	Ile	Ser	Arg	Val	Phe	Ile	Ala	Thr	His	Phe	Pro
				165					170					175	
His	Gln	Val	Ile	Leu	Gly	Val	Ile	Gly	Gly	Met	Leu	Val	Ala	Glu	Ala
			180					185					190		
Phe	Glu	His	Thr	Pro	Gly	Val	His	Met	Ala	Ser	Leu	Ser	Val	Tyr	Leu
		195					200					205			
Lys	Thr	Asn	Val	Phe	Leu	Phe	Leu	Phe	Ala	Leu	Gly	Phe	Tyr	Leu	Leu
	210					215					220				
Leu	Arg	Leu	Phe	Gly	Ile	Asp	Leu	Leu	Trp	Ser	Val	Pro	Ile	Ala	Lys
225					230					235					240
Lys	Trp	Cys	Ala	Asn	Pro	Asp	Trp	Ile	His	Ile	Asp	Ser	Thr	Pro	Phe
				245					250					255	
Ala	Gly	Leu	Val	Arg	Asn	Leu	Gly	Val	Leu	Phe	Gly	Leu	Gly	Phe	Ala
			260					265					270		
Ile	Asn	Ser	Glu	Met	Phe	Leu	Arg	Ser	Cys	Gln	Gly	Glu	Asn	Gly	Thr
		275					280					285			
Lys	Pro	Ser	Phe	Arg	Leu	Leu	Cys	Ala	Leu	Thr	Ser	Leu	Thr	Thr	Met
	290					295					300				
Gln	Leu	Tyr	Arg	Phe	Ile	Lys	Ile	Pro	Thr	His	Ala	Glu	Pro	Leu	Phe
305					310					315					320

Tyr Leu Leu Ser Phe Cys Lys Ser Ala Ser Ile Pro Leu Met Val Val
 325 330 335

Ala Leu Ile Pro Tyr Cys Val His Met Leu Met Arg Pro Gly Asp Lys
 340 345 350

Lys Thr Lys
 355

<210> 5
 <211> 14
 <212> PRT
 <213> Mus sp.

<220>
 <221> MISC_FEATURE
 <222> (2)..(2)
 <223> x = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (5)..(5)
 <223> x = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (10)..(10)
 <223> x = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (13)..(13)
 <223> x = any amino acid

<400> 5

Lys Xaa Arg Pro Xaa Pro Ser Gly His Xaa Ser Arg Xaa His
 1 5 10

<210> 6
 <211> 9
 <212> PRT
 <213> Mus sp.

<400> 6

Val Tyr Leu Lys Thr Asn Val Phe Leu
 1 5

<210> 7
 <211> 9
 <212> PRT
 <213> Artificial sequence

<220>

<223> artificial Mus sp.

<400> 7

Lys Tyr Asn Lys Ala Asn Val Phe Leu
1 5